

functional domains from genomic DNA or cDNA derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on

(i) the presence or absence of a mutation, and

(ii) whether the patient is node positive or not; and

d) prognosticating the development of the neoplasia by combining the results of steps c)(i) and c)(ii) and providing guidance for the treatment of the patient.

2. (Three Times Amended) The method of claim 1, further comprising the step of typing the mutation of step c)(ii) into a group selected from the group consisting of a missense mutation, a nonsense mutation, a deletion, and an insertion.

3. (Twice Amended) The method of claim 2, further comprising determining the presence and position of the mutation and categorizing biological aggressiveness and/or metastatic potential of the neoplasia based upon the presence, position, and type of mutation,

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wherein said neoplasia is breast cancer.

H4
4. (Three Times Amended) The method of claim 1 wherein
a an exon or exons of the sequenced nucleic acid encode a DNA
binding domain.

H5
5. (Twice Amended) The method of claim 1 wherein
evolutionary conserved regions of the nucleic acid are analyzed.

H6
7. (Twice Amended) The method of claim 6, wherein said
neoplasia originates from a breast neoplasia.

H7
10. (Three Times Amended) The method of claim 1, wherein
step a) is carried out using an automated nucleic acid sequencer,
computer software optionally being used to (i) track samples and
control process steps and/or (ii) to aid in and/or interpret
sequence data obtained.

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14. (Three Times Amended) A method for prognostication of
the development of neoplasia in a human patient having a
neoplasia comprising:

a) determining the nucleotide sequence of all exons of a cancer-related p53 nucleic acid which encode biologically functional domains from genomic DNA or cDNA derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on

(i) the presence or absence of a mutation, and

(ii) whether the patient is node positive or not; and

d) prognosticating the development of the neoplasia by combining the results of steps c) (i) and c) (ii).

15. (Three Times Amended) A method for prognostication of the development of neoplasia in a human patient having a neoplasia comprising:

a) determining the nucleotide sequence of all exons of a cancer-related p53 nucleic acid which encode biologically functional domains from genomic DNA or cDNA derived from a human neoplastic tissue or body fluid;

b) analyzing the entire nucleotide sequence determined in step a) for the presence of mutations; and

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c) classifying the neoplasia into different subgroups
depending on the presence or absence of a mutation; and

d) prognosticating the development of the neoplasia by
analyzing the results of step c) only.
